

# Hernández Mar- a Luisa

## List of Publications by Year in descending order

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20  
papers

695  
citations

687363

13  
h-index

752698

20  
g-index

22  
all docs

22  
docs citations

22  
times ranked

1481  
citing authors

#	ARTICLE	IF	CITATIONS
1	Candida albicans Hyphal Extracellular Vesicles Are Different from Yeast Ones, Carrying an Active Proteasome Complex and Showing a Different Role in Host Immune Response. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	13
2	Enrichment of ATP Binding Proteins Unveils Proteomic Alterations in Human Macrophage Cell Death, Inflammatory Response, and Protein Synthesis after Interaction with <i>Candida albicans</i> . <i>Journal of Proteome Research</i> , 2019, 18, 2139-2159.	3.7	3
3	SILAC-based phosphoproteomics reveals new PP2A-Cdc55-regulated processes in budding yeast. <i>GigaScience</i> , 2018, 7, .	6.4	24
4	Unraveling <i>Gardnerella vaginalis</i> Surface Proteins Using Cell Shaving Proteomics. <i>Frontiers in Microbiology</i> , 2018, 9, 975.	3.5	7
5	Identification of the Missing Protein Hyaluronan Synthase 1 in Human Mesenchymal Stem Cells Derived from Adipose Tissue or Umbilical Cord. <i>Journal of Proteome Research</i> , 2018, 17, 4325-4328.	3.7	6
6	A multicentric study to evaluate the use of relative retention times in targeted proteomics. <i>Journal of Proteomics</i> , 2017, 152, 138-149.	2.4	9
7	Quantitative differential proteomics of yeast extracellular matrix: there is more to it than meets the eye. <i>BMC Microbiology</i> , 2015, 15, 271.	3.3	14
8	<i>Candida albicans</i> Shaving to Profile Human Serum Proteins on Hyphal Surface. <i>Frontiers in Microbiology</i> , 2015, 6, 1343.	3.5	43
9	<i>Candida albicans</i> cell shaving uncovers new proteins involved in cell wall integrity, yeast to hypha transition, stress response and host-pathogen interaction. <i>Journal of Proteomics</i> , 2015, 127, 340-351.	2.4	68
10	In Vitro Transcription/Translation System: A Versatile Tool in the Search for Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3441-3451.	3.7	11
11	Methodologies to generate, extract, purify and fractionate yeast ECM for analytical use in proteomics and glycomics. <i>BMC Microbiology</i> , 2014, 14, 244.	3.3	11
12	General Statistical Framework for Quantitative Proteomics by Stable Isotope Labeling. <i>Journal of Proteome Research</i> , 2014, 13, 1234-1247.	3.7	165
13	Surfing Transcriptomic Landscapes. A Step beyond the Annotation of Chromosome 16 Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 158-172.	3.7	26
14	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013, 95, 84-88.	2.4	46
15	Dual Regulation of the Mitotic Exit Network (MEN) by PP2A-Cdc55 Phosphatase. <i>PLoS Genetics</i> , 2013, 9, e1003966.	3.5	23
16	Phosphoproteomic Analysis of Protein Kinase C Signaling in <i>Saccharomyces cerevisiae</i> Reveals Slit2 Mitogen-activated Protein Kinase (MAPK)-dependent Phosphorylation of Eisosome Core Components. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 557-574.	3.8	52
17	Quantitative Proteome and Acidic Subproteome Profiling of <i>Candida albicans</i> Yeast-to-Hypha Transition. <i>Journal of Proteome Research</i> , 2011, 10, 502-517.	3.7	41
18	Gel and gel-free proteomics to identify <i>Saccharomyces cerevisiae</i> cell surface proteins. <i>Journal of Proteomics</i> , 2010, 73, 1183-1195.	2.4	46

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19	Identification of <i>Candida albicans</i> exposed surface proteins in vivo by a rapid proteomic approach. <i>Journal of Proteomics</i> , 2010, 73, 1404-1409.	2.4	58
20	Combined Proteomic Approaches for the Identification of Specific Amino Acid Residues Modified by 4-Hydroxy-2-Nonenal under Physiological Conditions. <i>Journal of Proteome Research</i> , 2010, 9, 5770-5781.	3.7	24